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 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250
 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300
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1. DNA polymerase alpha (pol alpha) is a DNA polymerase that is involved in DNA replication. It is a large, multi-subunit enzyme that is found in the nucleus of eukaryotic cells. It is responsible for synthesizing the leading strand of DNA during replication. It is a member of the DNA polymerase family, which includes DNA polymerase beta, gamma, delta, and epsilon. It is a key enzyme in the DNA replication process.

2. The sequence of the DNA polymerase alpha gene is 1,203 base pairs long. It is located on chromosome 10. The gene is transcribed into a single mRNA molecule, which is then translated into a protein. The protein is composed of 401 amino acids. It is a monomeric enzyme.

3. The DNA polymerase alpha gene is located on chromosome 10. It is a large gene, with a total length of 1,203 base pairs. The gene is transcribed into a single mRNA molecule, which is then translated into a protein. The protein is composed of 401 amino acids. It is a monomeric enzyme.

4. The DNA polymerase alpha gene is located on chromosome 10. It is a large gene, with a total length of 1,203 base pairs. The gene is transcribed into a single mRNA molecule, which is then translated into a protein. The protein is composed of 401 amino acids. It is a monomeric enzyme.

5. The DNA polymerase alpha gene is located on chromosome 10. It is a large gene, with a total length of 1,203 base pairs. The gene is transcribed into a single mRNA molecule, which is then translated into a protein. The protein is composed of 401 amino acids. It is a monomeric enzyme.

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[illegible][illegible]

alpha 1,4-galactosyltransferase.
C.R. Soroka.

Phylum: Chordata; **Class:** Mammalia; **Order:** Carnivora; **Suborder:** Caniformia; **Family:** Felidae; **Genus:** *Felis*; **Species:** *Felis concolor*.

[illegible]

TITLE DNA sequence and chromosome localization of pta alpha 1.5
Gustafsson, K.
galactosyltransferase

JOURNAL
IMMUNOGENETICS 4: (2-3), 191-195 (1995)
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FEATURES
LOCATION/QUANTITIES
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SOURCE
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195
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/oden, start = i
/alpha = start;

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/db_xref="316426"

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1. The first step in the process of identifying a problem is to recognize that a problem exists. This is often done by comparing current performance with a desired state or goal. If there is a significant difference, a problem is identified.

THE UNIVERSITY OF CHICAGO

DATE COUNT 394 3 260 C 207 q 072 7
 DISSEMINATION OF INFORMATION IN THE U.S.S.R.
 BY THE KGB

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	ratio: 5.431	gaps: 0

Percent Similarity: 100.00% Percent Identity: 100.00%

attachment_point:
ncn-004-001-16 x p1001A

ALBUQUE 1/1 TO: PIKASTA FROM: I TO: L269

I W. A. ALBUQUERQUE, A. ALBUQUERQUE, S. MELLON, V. L. SOLARI, Y. F.

6. Δ GTGAATGGTCACCAAGAGATGGTCTGCTCAATGGTCTCTGTCTCAATAGTCTGCTG

17. ModelValValPhotSpotting [EASUSoftPac] - 01/18/96 01:00:00

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34 CTGTTCTCCCTGCCTGCTCATGCTGAGGCTGCTGCTGCTGCTGCTGCTGCT

[illegible][illegible]

376 TGGTACTTCTCCGAGCTGGTCTTAACAAAGGACATATATATTAACAGGAGA 215

Downloaded from <http://ajph.org/> on November 10, 2014









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Maximum number of iterations using sq model

Run for October 19, 2000, 12:14:14 Search time 2166.23 seconds
(without all updates)
1 to 100 million cell updates/sec

Iteration 08-08-04 400-7

Iteration 1112

Search for 1000000 iterations (1000000 iterations)

Search for 1000000 iterations (1000000 iterations)

Search for 1000000 iterations (1000000 iterations)

1429728

Maximum number of iterations

Maximum number of iterations

Post processing: Minimum Match 0%

Maximum Match 100%

Iteration 1st 45, Summary 45

Database

EST:

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[illegible]



[illegible][illegible]



[illegible][illegible]

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Harwell-Black, M.D., Ph.D.
cDNA Library Preparation: M. Ben-Soussan, Ph.D.
cDNA Library Arrayed By: Ben-Soussan, Ph.D.
cDNA Sequencing By: Washington University Genome Sequencing Center
cDNA Distribution: NCI-60 cell line distribution information can be
found through the LNC-A5 Home Site/ Distribution/ LNC-A5
Web Page: <http://www.nci.nih.gov/ncicb/nci60/>
Source: 4000 clones from cDNA
Library/Qualifications
1. 442

Organism: "Homo sapiens"
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/clone: "HAG12285"
/clone_lib: "NCI-60 cell line"
/sex: "male"
/cell_type: "adipocyte"
/lab_host: "DH10B"
/notes: "Original host: Vector: p1140 Pac (Pharmacia)
with a modified polylinker. Plasmid DNA from the
normalized library NCI-60_12285 was prepared, and ss
cloned were made. The following GAP purification
this DNA was used as a probe in a subtractive hybridization
reaction. The driver was 17x-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonets
45668-96679, 13172-133459, and 121928-122065)."
Submitted by: Ben-Soussan and M. Fatima Bonafide.

FASTA: UNI 08.4 227 c 803 100 1 1 others
41118
Query: M1200 1.000 Score: 9.180 E-124 Ident: 142
Best match: Similarity: 73.9% Pos: 85-121
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1 GENERAL INFORMATION
2 ADDRESS: 1500 JEFFERSON HWY, SUITE 400
3 TITLE OF INVENTION: Method and Products for the Synthesis of
4 Oligosaccharide Structures on Glycoproteins, Glycolipids,
5 TITLE OF INVENTION: or as Free Molecules, and for the Isolation of Cloned
6 TITLE OF INVENTION: Genetic Sequences that Determine these Structures
7 NUMBER OF SEQUENCES: 16
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: JOHN SPIVAK, MONTPELLIER, MA 01801
10 ADDRESS: P.O.
11 STREET: 1755 Jefferson Davis Highway, Suite 400
12 CITY: Arlington
13 STATE: Virginia
14 ZIP: 22202
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: MS-DOS/MS-DOS
19 SOFTWARE: Patent in Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 FILING DATE: 1991-02-14
22 CLASSIFICATION: 46
23 AGENT/AGENT INFORMATION:
24 NAME: Leavitts Ph.D., Joan Paul
25 REGISTRATION NUMBER: 31,451
26 REFERENCE/PATENT NUMBER: 2,463,021 55, 401
27 TELEPHONE: (703) 521-5946
28 TELEFAX: (703) 521-5946
29 INDEX: 2463-021-5946
30 INFORMATION FOR SEQ ID NO: 1
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 404 amino acids
33 TYPE: AMINO ACID
34 STRANDINGS: Single
35 POSITIVE: 100%
36 INFORMATION: YES
37 ORIGINAL SOURCE:
38 SOURCE TYPE: 100%
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Web: mads@protonmail.com

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State: TX

Zip: 77006

Country: USA

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Fax: 713 500 5439

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Web: mads@protonmail.com

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City: Houston

State: TX

Zip: 77006

Country: USA

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Fax: 713 500 5439

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Web: mads@protonmail.com

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Zip: 77006

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City: Houston

State: TX

Zip: 77006

Country: USA

Phone: 713 500 5437

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Email: mads@protonmail.com

Web: mads@protonmail.com






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1  ADDRESS: 1000 N. JEFFERSON, BOSTON, MA 02115, U.S.A.
2  SERIAL: 1000 Jefferson Davis Highway, Fourth Floor
3  CITY: Arlington
4  STATE: Virginia
5  COUNTRY: U.S.A.
6  DATE: 22/02/00
7  COMPUTER RELEASABLE FORM:
8  COMPILE TYPE: floppy disk
9  COMPILE: IBM PC compatible
10  OPERATOR: JIM J. JONES
11  SOFTWARE: Patent in Release #10, Version #1.25
12  COMPUTER APPLICATION DATA:
13  TITLE: IN INVENTION
14  FILE NAME: 1000 Jefferson Davis Highway
15  CLASSIFICATION: 4.0
16  ALL INDICATED INFORMATION:
17  NAME: Jones, Jim Paul M. Jr.
18  REGISTRATION NUMBER: 1000
19  PREFERENCE: 1000
20  REFERENCE: 1000
21  TELEPHONE: (703) 521-4500
22  TELEFAX: (703) 521-4500
23  INDEX: 240000, 240000
24  INFORMATION FOR SEQ ID NO: 1
25  SEQUENCE CHARACTERISTICS:
26  LENGTH: 1000 base pairs
27  TYPE: nucleic acid
28  STRANDEDNESS: single
29  ORIENTATION: 5' to 3'
30  ANALYSIS: N/A
31  ANALYSIS: N/A
32  ANALYSIS: N/A

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1  QUALITY: 100.00
2  Gaps: 4
3  Percent Similarity: 99.97% Percent Identity: 72.65%

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1  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000
2  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000
3  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000

```

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1  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000
2  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000
3  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000

```

```

1  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000
2  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000
3  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000

```

```

1  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000
2  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000
3  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000

```

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1  seq_name: 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000

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1  seq_documentation:

```

```

1  seq_documentation: 05/08/94/41

```

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1  Patent No. 5,455,417

```

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1  GENERAL INFORMATION:

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1  APPLICANT: JAMES J. JONES

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1  TITLE OF INVENTION: METHOD AND APPARATUS FOR THE SYNTHESIS

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1  OF POLYMERIZABLE SUBSTANCES ON POLYMERIZABLE

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1  TITLE OF INVENTION: POLYMERIZABLE SUBSTANCES ON POLYMERIZABLE

```


[illegible]



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all protein protein scores against 884411
 October 19, 2000, 12:00:44 : Search time 11.69 seconds
 (without alignment)
 1016.916 million cell updates/sec

100 best protein scores
 2016
 US 08 984 900 10
 1016.916 million cell updates/sec

Sequence
 1016.916 million cell updates/sec

Sequence table
 1016.916 million cell updates/sec

Sequence
 1016.916 million cell updates/sec

Sequence
 1016.916 million cell updates/sec

Sequence
 1016.916 million cell updates/sec

Sequence
 1016.916 million cell updates/sec

Sequence
 1016.916 million cell updates/sec

100 best protein scores
 2016
 US 08 984 900 10
 1016.916 million cell updates/sec

SUMMARY

Protein No.	Score	Query	Match	Length	ID	Description
1	2016	100.0	921	1	GATK_P13	P54127 SUS SCRODA
2	1777.6	88.2	368	1	GATK_P13	P14769 SUS SCRODA
3	1740	74.9	344	1	GATK_P13	P21106 SUS SCRODA
4	1606.5	31.7	354	1	GATK_P13	P16442 SUS SCRODA
5	96.5	4.8	569	1	GATK_P13	P01920 SUS SCRODA
6	94	4.7	106	1	GATK_P13	P01920 SUS SCRODA
7	94	4.6	106	1	GATK_P13	P01920 SUS SCRODA
8	90.5	4.5	7.6	1	GATK_P13	P24110 SUS SCRODA
9	89	4.4	7.6	1	GATK_P13	P24110 SUS SCRODA
10	88	4.3	204	1	GATK_P13	P16924 SUS SCRODA
11	87	4.3	400	1	GATK_P13	P16924 SUS SCRODA
12	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
13	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
14	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
15	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
16	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
17	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
18	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
19	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
20	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
21	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
22	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
23	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
24	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
25	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
26	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
27	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
28	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
29	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
30	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
31	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
32	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
33	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
34	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA
35	86.3	4.2	740	1	GATK_P13	P16924 SUS SCRODA

34	82	4.1	885	1	YGLW_YEAST	P14774 SUS SCRODA
35	82	4.1	2009	1	YGLW_YEAST	P14774 SUS SCRODA
36	81.5	4.0	439	1	YGLW_YEAST	P14774 SUS SCRODA
37	81.5	4.0	1559	1	YGLW_YEAST	P14774 SUS SCRODA
38	81	4.0	396	1	YGLW_YEAST	P14774 SUS SCRODA
39	81	4.0	505	1	YGLW_YEAST	P14774 SUS SCRODA
40	81	4.0	643	1	YGLW_YEAST	P14774 SUS SCRODA
41	81	4.0	1159	1	YGLW_YEAST	P14774 SUS SCRODA
42	80.7	4.0	445	1	YGLW_YEAST	P14774 SUS SCRODA
43	80.5	4.0	519	1	YGLW_YEAST	P14774 SUS SCRODA
44	80.5	4.0	853	1	YGLW_YEAST	P14774 SUS SCRODA
45	80	4.0	510	1	YGLW_YEAST	P14774 SUS SCRODA

ALIGNMENTS

34	82	4.1	885	1	YGLW_YEAST	P14774 SUS SCRODA
35	82	4.1	2009	1	YGLW_YEAST	P14774 SUS SCRODA
36	81.5	4.0	439	1	YGLW_YEAST	P14774 SUS SCRODA
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